

WEST Search History

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DATE: Thursday, November 03, 2005

[Hide?](#) [Set Name](#) [Query](#)

[Hit Count](#)

DB=PGPB,USPT,EPAB; PLUR=YES; OP=OR

<input type="checkbox"/> L51	L50 and l17	2
<input type="checkbox"/> L50	(424/179.1)![CCLS]	249
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<input type="checkbox"/> L46	L45 and L44	1
<input type="checkbox"/> L45	cancer\$ or tumor\$ or neoplas\$	175849
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<input type="checkbox"/> L42	L41 or L40 or L38	267
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<input type="checkbox"/> L39	L37.ti	3560
<input type="checkbox"/> L38	L37.ab.	31
<input type="checkbox"/> L37	dota	3560
<input type="checkbox"/> L36	L34 or L35	2631
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<input type="checkbox"/> L21	L20 with L2	551

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<input type="checkbox"/>	L19	?antibod?	132
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<input type="checkbox"/>	L5	L4 not @py>2003	254
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<input type="checkbox"/>	L1	antibod?	126273

END OF SEARCH HISTORY

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:19:05 ; Search time 120 Seconds
(without alignments)
702.615 Million cell updates/sec

Title: US-09-671-953B-5

Perfect score: 1132

Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
<hr/>						
1	1130	99.8	218	4	AAB20358	Aab20358 Anti-chel
2	1118	98.8	218	4	AAB20359	Aab20359 Anti-chel
3	1113	98.3	218	4	AAB20360	Aab20360 Anti-chel
4	1079	95.3	218	8	ADQ98050	Adq98050 Chimeric
5	1078	95.2	218	8	ADQ98051	Adq98051 Chimeric
6	776	68.6	215	8	ADR23362	Adr23362 Human CD7
7	759	67.0	235	2	AAW82740	Aaw82740 Plasmid p
8	755.5	66.7	235	5	AAE27925	Aae27925 Human C2B
9	755.5	66.7	235	6	ABB82834	Abb82834 Antibody

10	755	66.7	213	8	ADL92471	Adl92471 Antibody
11	751	66.3	220	2	AAW07528	Aaw07528 Anti-HGF
12	750.5	66.3	235	3	AAB08025	Aab08025 A dimeric
13	749.5	66.2	234	5	AAO14066	Aao14066 Light cha
14	749.5	66.2	234	6	ABU08018	Abu08018 Human mon
15	749.5	66.2	234	7	ADF65776	Adf65776 Human mon
16	749.5	66.2	234	8	ADJ92516	Adj92516 Human SOJ
17	749	66.2	213	6	AAE34878	Aae34878 BIWA4/8 a
18	749	66.2	213	8	ADL15445	Adl15445 Humanised
19	749	66.2	213	8	ADO00853	Ado00853 Humanised
20	747	66.0	213	6	AAE35326	Aae35326 Humanised
21	747	66.0	213	6	AAE34877	Aae34877 BIWA4 ant
22	747	66.0	213	8	ADL15441	Adl15441 Humanised
23	747	66.0	213	8	ADO00849	Ado00849 Humanised
24	746	65.9	215	8	ADQ31891	Adq31891 Antibody
25	746	65.9	239	8	ADK70470	Adk70470 Respirato
26	745.5	65.9	240	6	ABJ38595	Abj38595 Hepatitis
27	744	65.7	215	8	ADQ31885	Adq31885 Antibody
28	742	65.5	215	8	ADQ16702	Adq16702 Modified
29	742	65.5	236	8	ADP79579	Adp79579 Chimeric
30	741.5	65.5	234	3	AAY92239	Aay92239 Human bon
31	741	65.5	236	2	AAY34096	Aay34096 Partial a
32	740	65.4	213	4	AAB83157	Aab83157 Gangliosi
33	740	65.4	233	3	AAY93704	Aay93704 The kappa
34	740	65.4	233	3	AAY93731	Aay93731 The kappa
35	740	65.4	233	6	AAE35886	Aae35886 Human 4.8
36	739.5	65.3	214	2	AAY08599	Aay08599 Anti-huma
37	739	65.3	241	6	ABJ38593	Abj38593 Hepatitis
38	738.5	65.2	234	6	ABP55483	Abp55483 CJRA05 pr
39	738.5	65.2	240	6	ABJ38594	Abj38594 Hepatitis
40	738	65.2	235	2	AAW06180	Aaw06180 Humanised
41	737.5	65.2	214	8	ADH34591	Adh34591 023 light
42	737	65.1	213	2	AAW05830	Aaw05830 Humanised
43	737	65.1	215	6	ABR01469	Abr01469 Human ant
44	736.5	65.1	216	8	ADS87940	Ads87940 Anti-IFN-
45	736.5	65.1	216	8	ADS94937	Ads94937 Anti-IFN-

ALIGNMENTS

RESULT 1

AAB20358

ID AAB20358 standard; protein; 218 AA.

XX

AC AAB20358;

XX

DT 11-JUN-2001 (first entry)

XX

DE Anti-chelate antibody CHA255 light chain mutant N96C.

XX

KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;
KW cancer; therapy; mutant; mutein.

XX

OS Mus musculus.

OS Synthetic.

XX

FH Key Location/Qualifiers
FT Region 1. .23
FT /label= FR1
FT /note= "framework region 1"
FT Region 24. .37
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 38. .52
FT /label= FR2
FT /note= "framework region 2"
FT Region 53. .59
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 60. .92
FT /label= FR3
FT /note= "framework region 3"
FT Region 93. .100
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FT Region 101. .131
FT /label= FR4
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FT Misc-difference 112
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FT Misc-difference 207
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XX
PN WO200122922-A2.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-US026619.
XX
PR 27-SEP-1999; 99US-0156194P.
PR 31-MAY-2000; 2000US-0208684P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Meares C, Chmura A;
XX
DR WPI; 2001-244971/25.
DR N-PSDB; AAF30633.
XX
PT Nucleic acid encoding a mutant antibody comprising a reactive site that
PT specifically binds to a metal chelate useful as analytical agents and in
PT clinical diagnosis, as well as in the treatment of disease, particularly
PT cancer.
XX
PS Disclosure; Fig 12; 100pp; English.

XX
CC The invention provides a mutant antibody comprising a reactive site that
CC is not present in the wild-type of the antibody. The antibody also has a
CC complementarity determining region (CDR) that specifically binds to a
CC metal chelate against which the wild-type antibody is raised. The
CC reactive site of the mutant antibody is in a position proximate to or
CC within the CDR, such that the chelate and the antibody are able to form a
CC covalent bond. The present sequence is that of the light chain variable
CC region of anti-indium-EDTA monoclonal antibody CHA255, carrying an N96C
CC mutation. As an example of the method of the invention, rational computer
CC -aided design was used to develop an indium-EDTA chelate to covalently
CC bind to CHA255 in vivo. The premise was to allow the chelate to bind non-
CC covalently to CHA255 bound to a tumour and then to covalently attach the
CC chelate to the antibody, thereby trapping it at the tumour site. This
CC involved cloning the variable domains of CHA255 to construct a
CC human/mouse chimeric Fab fragment that could be expressed in Escherichia
CC coli, and the synthesis and screening of benzyl-EDTA chelates carrying
CC weakly electrophilic groups capable of conjugation of the antibody in
CC vivo. This Fab can be conjugated to a targeting moiety when desired. A
CC reactive site was incorporated into the antibody by engineering a Cys
CC residue at location Asn-96 or Ser-95 of the light chain, near the region
CC of the antibody to which the chelate bound. This was accomplished by site
CC -directed mutagenesis of a nucleic acid encoding the wild-type of the
CC anti-chelate antibody

XX

SQ Sequence 218 AA;

Query Match 99.8%; Score 1130; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 7.4e-80;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPG 60
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Db 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPG 60

Qy 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
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Db 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120

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Qy 181 STLTLSKADYEKKVYACEVTHQGLSXPVTKSFNRGEC 218

||||||||||||||||||||||||||||||||

Db 181 STLTLSKADYEKKVYACEVTHQGLSXPVTKSFNRGEC 218

RESULT 2

AAB20359

ID AAB20359 standard; protein; 218 AA.

XX

AC AAB20359;

XX

DT 11-JUN-2001 (first entry)

XX

DE Anti-chelate antibody CHA255 light chain.

XX
KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;
KW cancer; therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 1. .23
FT /label= FR1
FT /note= "framework region 1"
FT Region 24. .37
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 38. .52
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FT Region 53. .59
FT /label= CDR2
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PN WO200122922-A2.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-US026619.
XX
PR 27-SEP-1999; 99US-0156194P.
PR 31-MAY-2000; 2000US-0208684P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Meares C, Chmura A;
XX
DR WPI; 2001-244971/25.
DR N-PSDB; AAF30634.
XX
PT Nucleic acid encoding a mutant antibody comprising a reactive site that
PT specifically binds to a metal chelate useful as analytical agents and in

PT clinical diagnosis, as well as in the treatment of disease, particularly
PT cancer.
XX
PS Disclosure; Fig 13; 100pp; English.
XX
CC The invention provides a mutant antibody comprising a reactive site that
CC is not present in the wild-type of the antibody. The antibody also has a
CC complementarity determining region (CDR) that specifically binds to a
CC metal chelate against which the wild-type antibody is raised. The
CC reactive site of the mutant antibody is in a position proximate to or
CC within the CDR, such that the chelate and the antibody are able to form a
CC covalent bond. The present sequence is that of the light chain of anti-
CC indium-EDTA monoclonal antibody CHA255. As an example of the method of
CC the invention, rational computer-aided design was used to develop an
CC indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was
CC to allow the chelate to bind non-covalently to CHA255 bound to a tumour
CC and then to covalently attach the chelate to the antibody, thereby
CC trapping it at the tumour site. This involved cloning the variable
CC domains of CHA255 to construct a human/mouse chimeric Fab fragment that
CC could be expressed in Escherichia coli, and the synthesis and screening
CC of benzyl-EDTA chelates carrying weakly electrophilic groups capable of
CC conjugation of the antibody in vivo. This Fab can be conjugated to a
CC targeting moiety when desired. A reactive site was incorporated into the
CC antibody by engineering a Cys residue at location Asn-96 or Ser-95 of the
CC light chain, near the region of the antibody to which the chelate bound.
CC This was accomplished by site-directed mutagenesis of a nucleic acid
CC encoding the wild-type of the anti-chelate antibody
XX
SQ Sequence 218 AA;

Query Match 98.8%; Score 1118; DB 4; Length 218;
Best Local Similarity 99.5%; Pred. No. 6.4e-79;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSNLWVFGGGTKLTVLSRTVAAPSVF 120

Qy 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
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Qy 181 STLTLSKADYEHKVVACEVTHQGLSXPVTKSFNRGEC 218
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Db 181 STLTLSKADYEHKVVACEVTHQGLSXPVTKSFNRGEC 218

RESULT 3
AAB20360
ID AAB20360 standard; protein; 218 AA.
XX
AC AAB20360;
XX

DT 11-JUN-2001 (first entry)
XX
DE Anti-chelate antibody CHA255 light chain mutant S95C.
XX
KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;
KW cancer; therapy; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .23
FT /label= FR1
FT /note= "framework region 1"
FT Region 24. .37
FT /label= CDR1
FT /note= "complementarity determining region 1"
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PN WO200122922-A2.
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PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-US026619.
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PR 27-SEP-1999; 99US-0156194P.
PR 31-MAY-2000; 2000US-0208684P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Meares C, Chmura A;

XX
DR WPI; 2001-244971/25.
DR N-PSDB; AAF30635.
XX
PT Nucleic acid encoding a mutant antibody comprising a reactive site that
PT specifically binds to a metal chelate useful as analytical agents and in
PT clinical diagnosis, as well as in the treatment of disease, particularly
PT cancer.
XX
PS Disclosure; Fig 14; 100pp; English.
XX
CC The invention provides a mutant antibody comprising a reactive site that
CC is not present in the wild-type of the antibody. The antibody also has a
CC complementarity determining region (CDR) that specifically binds to a
CC metal chelate against which the wild-type antibody is raised. The
CC reactive site of the mutant antibody is in a position proximate to or
CC within the CDR, such that the chelate and the antibody are able to form a
CC covalent bond. The present sequence is that of the light chain variable
CC region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C
CC mutation. As an example of the method of the invention, rational computer
CC -aided design was used to develop an indium-EDTA chelate to covalently
CC bind to CHA255 in vivo. The premise was to allow the chelate to bind non-
CC covalently to CHA255 bound to a tumour and then to covalently attach the
CC chelate to the antibody, thereby trapping it at the tumour site. This
CC involved cloning the variable domains of CHA255 to construct a
CC human/mouse chimeric Fab fragment that could be expressed in Escherichia
CC coli, and the synthesis and screening of benzyl-EDTA chelates carrying
CC weakly electrophilic groups capable of conjugation of the antibody in
CC vivo. This Fab can be conjugated to a targeting moiety when desired. A
CC reactive site was incorporated into the antibody by engineering a Cys
CC residue at location Asn-96 or Ser-95 of the light chain, near the region
CC of the antibody to which the chelate bound. This was accomplished by site
CC -directed mutagenesis of a nucleic acid encoding the wild-type of the
CC anti-chelate antibody
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SQ Sequence 218 AA;

Query Match 98.3%; Score 1113; DB 4; Length 218;
Best Local Similarity 99.1%; Pred. No. 1.6e-78;
Matches 216; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPG 60
Db 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPG 60

Qy 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLVFGGGTKLTVLSRTVAAPSVF 120
Db 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTCLSRTVAAPSVF 120

Qy 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180

Qy 181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218

RESULT 4
ADQ98050
ID ADQ98050 standard; protein; 218 AA.
XX
AC ADQ98050;
XX
DT 21-OCT-2004 (first entry)
XX
DE Chimeric murine 2D12.5 variable light chain fused to human TTCL protein.
XX
KW murine; mouse; chimeric; human; TTCL; tetanus toxin;
KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
KW single photon emission tomography; SPET; cancer; cytostatic;
KW immunosuppressive; multi-functional antibody; metal chelate;
KW antigen recognition domain; in vivo imaging;
KW cell-antibody-metal chelate complex; emission tomography.
XX
OS Mus musculus.
OS Homo sapiens.
OS Chimeric.
XX
PN WO2004065569-A2.
XX
PD 05-AUG-2004.
XX
PF 23-JAN-2004; 2004WO-US001808.
XX
PR 23-JAN-2003; 2003US-00350555.
PR 22-JUL-2003; 2003US-00625047.
PR 31-JUL-2003; 2003US-00631258.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Meares C, Corneillie T;
XX
DR WPI; 2004-580725/56.
DR N-PSDB; ADQ98054.
XX
PT Novel mutant antibody comprising reactive site not present in wild-type
PT of antibody and antigen recognition domain that recognizes macrocyclic
PT metal chelate having four nitrogen atoms, useful for treating cancer or
PT autoimmune diseases.
XX
PS Claim 41; SEQ ID NO 27; 208pp; English.
XX
CC This invention relates to multi-functional antibodies that recognise
CC chelating agents and metal chelates, particularly macrocyclic metal
CC chelates. Specifically, it refers to an antibody that comprises a metal
CC chelate bound to an antigen recognition domain, where the metal chelate
CC has a reactive functional group of complementary reactivity to the
CC reactive site of the antibody. This reactive site is the side chain of a
CC naturally occurring amino acid e.g. the -SH group side chain of a
CC cysteine residue (not present in the wild type) which can be used to form
CC a covalent bond between the reactive site of the antibody and the
CC reactive functional group of the metal chelate. The present invention
CC describes using these antibodies for in vivo imaging where the antibody

CC comprises a targeting moiety that binds specifically to a cell via a cell
CC surface receptor or antigen thus forming a cell-mutant antibody complex.
CC On addition of the metal chelate, a cell-antibody-metal chelate complex
CC is formed that can be detected using emission tomography, magnetic
CC resonance imaging, lanthanide luminescence, gamma-emissions or single
CC photon emission tomography (SPET). As such, this method is useful for
CC treating a subject with cancer and pharmaceutical compositions exhibit
CC cytostatic and immunosuppressive activities. This polypeptide sequence is
CC the chimeric murine antibody 2D12.5 variable light chain protein fused to
CC the human anti-tetanus toxin antibody kappa light chain constant region
CC of the invention.

XX

SQ Sequence 218 AA;

Query Match 95.3%; Score 1079; DB 8; Length 218;
Best Local Similarity 95.9%; Pred. No. 6.8e-76;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 RSAVVTQESALTTSPGETVLTCCRSSLGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPG 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 RSAVVTQESALTTSPGETVLTCCRSSLGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPG 60

Qy 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 VPARFSGSLIGDKAALTIAAGTQTEDEAIYFCALWYSNHWFGGGTKLTVLSRTVAAPSVF 120

Qy 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180

Qy 181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218

||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218

RESULT 5

ADQ98051

ID ADQ98051 standard; protein; 218 AA.

XX

AC ADQ98051;

XX

DT 21-OCT-2004 (first entry)

XX

DE Chimeric N53C murine 2D12.5 light chain variable and human TTCL protein.

XX

KW murine; mouse; chimeric; human; TTCL; tetanus toxin;
KW magnetic resonance imaging; lanthanide luminescence; gamma-emissions;
KW single photon emission tomography; SPET; cancer; cytostatic;
KW immunosuppressive; multi-functional antibody; metal chelate;
KW antigen recognition domain; in vivo imaging;
KW cell-antibody-metal chelate complex; emission tomography; mutant; mutein.

XX

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

OS Synthetic.

XX

FH Key Location/Qualifiers
FT Misc-difference 55
FT /note= "Wild type Asn substituted for Cys"
XX
PN WO2004065569-A2.
XX
PD 05-AUG-2004.
XX
PF 23-JAN-2004; 2004WO-US001808.
XX
PR 23-JAN-2003; 2003US-00350555.
PR 22-JUL-2003; 2003US-00625047.
PR 31-JUL-2003; 2003US-00631258.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Meares C, Corneillie T;
XX
DR WPI; 2004-580725/56.
DR N-PSDB; ADQ98055.
XX
PT Novel mutant antibody comprising reactive site not present in wild-type
PT of antibody and antigen recognition domain that recognizes macrocyclic
PT metal chelate having four nitrogen atoms, useful for treating cancer or
PT autoimmune diseases.
XX
PS Claim 41; SEQ ID NO 28; 208pp; English.
XX
CC This invention relates to multi-functional antibodies that recognise
CC chelating agents and metal chelates, particularly macrocyclic metal
CC chelates. Specifically, it refers to an antibody that comprises a metal
CC chelate bound to an antigen recognition domain, where the metal chelate
CC has a reactive functional group of complementary reactivity to the
CC reactive site of the antibody. This reactive site is the side chain of a
CC naturally occurring amino acid e.g. the -SH group side chain of a
CC cysteine residue (not present in the wild type) which can be used to form
CC a covalent bond between the reactive site of the antibody and the
CC reactive functional group of the metal chelate. The present invention
CC describes using these antibodies for in vivo imaging where the antibody
CC comprises a targeting moiety that binds specifically to a cell via a cell
CC surface receptor or antigen thus forming a cell-mutant antibody complex.
CC On addition of the metal chelate, a cell-antibody-metal chelate complex
CC is formed that can be detected using emission tomography, magnetic
CC resonance imaging, lanthanide luminescence, gamma-emissions or single
CC photon emission tomography (SPET). As such, this method is useful for
CC treating a subject with cancer and pharmaceutical compositions exhibit
CC cytostatic and immunosuppressive activities. This polypeptide sequence is
CC the chimeric mutant N53C murine antibody 2D12.5 variable light chain
CC protein fused to the human anti-tetanus toxin antibody kappa light chain
CC constant region of the invention.
XX
SQ Sequence 218 AA;

Query Match 95.2%; Score 1078; DB 8; Length 218;
Best Local Similarity 95.9%; Pred. No. 8.2e-76;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db      1 RSAVVTQESALTTSPGETVTLTCRSSSTGAVTTSNYANWVQEKPDLFTGLIGGCNNRPPG 60

Qy      61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCWVFGGGTKLTVLSRTVAAPSVF 120
        ||||||| ||||||| ||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWFGGGTKLTVLSRTVAAPSVF 120

Qy      121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
        ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |
Db      121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180

Qy      181 STTLSKADYEKHKVYACEVTHQGLXPVTKSFNRGEC 218
        ||||||| ||||||| ||||||| ||| | | | | | | | | | | | | | | | | |
Db      181 STTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218

```

RESULT 6

ADR23362

ID ADR23362 standard; protein; 215 AA.

XX

AC ADR23362;

XX

DT 04-NOV-2004 (first entry)

XX

DE Human CD72-targeted IgG1 light chain.

XX

KW Human; CD72; B-lymphocyte; receptor; scFv; antibody; cytostatic;

KW immuno suppressive; cancer; autoimmune disease; gene therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1. .109

FT /label= V_region

FT Region 110. .215

FT /label= C_region

XX

PN WO2004067569-A1.

XX

PD 12-AUG-2004.

XX

PF 27-JAN-2003; 2003WO-EP050004.

XX

PR 27-JAN-2003; 2003WO-EP050004.

XX

PA (CRUC-) CRUCELL HOLLAND BV.

XX

PI Bakker ABH, Marissen WE;

XX

DR WPI; 2004-580978/56.

DR N-PSDB; ADR23361.

XX

PT New internalizing human binding molecules capable of specifically binding to CD72, useful for diagnosing and/or treating B-cell associated

PT diseases, such as cancer or autoimmune disorders.

XX

PS Example 5; SEQ ID NO 54; 174pp; English.

xx

CC The present sequence is the protein sequence of the light chain of human
CC IgG1 antibody 025, which specifically recognises human B cell associated
CC antigen CD72. An scFv ADR23324 selected from an antibody phage display
CC library was shown to specifically recognise the human CD72 receptor. The
CC scFv was recloned in IgG expression vector C01 using primers designed to
CC restore complete human frameworks, thereby generating antibody 025. Such
CC anti-CD72 immunoglobulins or their antigen-binding fragments can be used
CC as internalising human binding molecules of the invention. These
CC internalising human binding molecules are capable of (specifically)
CC binding to CD72 or its antigenic determinant, and preferably bind to CD72
CC associated with cells. Upon binding to CD72 present on the surface of
CC target cells, the binding molecules internalise. In addition to the
CC internalising human binding molecules, the invention provides
CC immunoconjugates comprising an internalising human binding molecule and a
CC tag (toxic substance, radioactive substance, liposome and/or enzyme),
CC nucleic acids encoding these, and compositions comprising them. The
CC internalising human binding molecule, immunoconjugate, nucleic acid
CC molecule or composition can be used in the diagnosis and/or treatment of
CC a B cell associated disorder or disease, especially a B cell associated
CC cancer and B cell associated autoimmune disorder (claimed).

xx

SO Sequence 215 AA;

Query Match 68.6%; Score 776; DB 8; Length 215;
Best Local Similarity 73.5%; Pred. No. 2.4e-52;
Matches 161; Conservative 16; Mismatches 36; Indels 6; Gaps 3;

Qy 2 SAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLHFTGLIGGTNNRAPGV 61
|: :||: |:: : |::| :||: | | | ||: |::| :| | :| | ||: |:
pb 1 SSELTODRAVSVALGOTVBRITCO---GDSIPLSYYASWYQOKRGOAPVILVLYGKNNRPSGT 52

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Qy      120 FIFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
       ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db      117 FIFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 176

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Qy	180	SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC	218
Db	177	SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	215

us-09-671-953b-5.rai

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:23:21 ; Search time 30 Seconds
(without alignments)
542.450 Million cell updates/sec

Title: US-09-671-953B-5

Perfect score: 1132

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	751	66.3	220	3	US-08-952-235-1	Sequence 1, Appl
3	751	66.3	220	4	US-09-669-971-1	Sequence 1, Appl
4	740	65.4	233	4	US-09-472-087-15	Sequence 15, Appl
5	740	65.4	233	4	US-09-472-087-67	Sequence 67, Appl
6	738	65.2	235	4	US-09-011-769A-27	Sequence 27, Appl
7	735	64.9	213	3	US-08-397-411-12	Sequence 12, Appl
8	734.5	64.9	491	4	US-10-011-125A-2	Sequence 2, Appl
9	734	64.8	236	4	US-09-315-926A-79	Sequence 79, Appl
10	732	64.7	235	4	US-09-472-087-14	Sequence 14, Appl
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14	730.5	64.5	224	4	US-09-453-234-84	Sequence 84, Appl
15	729.5	64.4	234	4	US-09-472-087-17	Sequence 17, Appl
16	729.5	64.4	234	4	US-09-472-087-69	Sequence 69, Appl
17	728.5	64.4	224	4	US-09-456-090A-46	Sequence 46, Appl

us-09-671-953b-5.ra1						
18	728.5	64.4	224	4	US-09-453-234-46	Sequence 46, App1
19	728.5	64.4	234	4	US-09-740-002-24	Sequence 24, App1
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21	727	64.2	233	3	US-09-485-737B-69	Sequence 69, App1
22	727	64.2	233	4	US-10-071-485-69	Sequence 69, App1
23	726	64.1	235	3	US-09-171-945-17	Sequence 17, App1
24	725.5	64.1	224	4	US-09-456-090A-36	Sequence 36, App1
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27	725.5	64.1	226	4	US-09-453-234-74	Sequence 74, App1
28	724.5	64.0	214	3	US-09-247-352-4	Sequence 4, Appli
29	724.5	64.0	214	4	US-09-466-635-4	Sequence 4, Appli
30	723.5	63.9	213	3	US-08-630-820-6	Sequence 6, Appli
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32	723.5	63.9	236	1	US-08-157-101A-5	Sequence 5, Appli
33	723	63.9	219	3	US-09-027-449-72	Sequence 72, App1
34	723	63.9	219	3	US-09-026-985-72	Sequence 72, App1
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36	723	63.9	219	4	US-09-234-340A-72	Sequence 72, App1
37	723	63.9	239	4	US-09-627-896B-22	Sequence 22, App1
38	723	63.9	242	3	US-09-027-449-56	Sequence 56, App1
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45	722	63.8	214	3	US-08-437-642B-24	Sequence 24, App1

ALIGNMENTS

RESULT 1

US-09-423-439-18

Sequence 18, Application US/09423439

Patent No. 6339070

GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles

TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439

FILING DATE: 09-No. 6339070-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294

FILING DATE: 05-MAY-1998

APPLICATION NUMBER: GB 9709421.3

FILING DATE: 10-MAY-1997

us-09-671-953b-5.raii

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-423-439-18

Query Match 67.0%; Score 759; DB 3; Length 235;
Best Local Similarity 72.2%; Pred. No. 1.6e-67;
Matches 156; Conservative 15; Mismatches 39; Indels 6; Gaps 3;

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us-09-671-953b-5.rapb

GenCore version 5.1.6
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SUMMARIES

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9	755	66.7	213	17	US-10-822-231-3	Sequence 3, Appl	
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19	749	66.2	213	16	US-10-704-522-8	Sequence 8, Appl	
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26	746	65.9	215	17	US-10-724-274-32	Sequence 32, Appl	
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ALIGNMENTS

RESULT 1

US-10-625-047-27

; Sequence 27, Application US/10625047

; Publication No. US20040198962A1

GENERAL INFORMATION:

APPLICANT: Meares, Claude

APPLICANT: Corneillie, Todd

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Multi-Functional Antibodies

FILE REFERENCE: 023070-130910us

CURRENT APPLICATION NUMBER: US/10/625,047

CURRENT FILING DATE: 2003-07-22

PRIOR APPLICATION NUMBER: US 10/350,555

PRIOR FILING DATE: 2003-01-23

us-09-671-953b-5.rapb

NUMBER OF SEQ ID NOS: 72
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SEQ ID NO 27
LENGTH: 218
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:native cloned
OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region
OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody
OTHER INFORMATION: kappa light chain constant region (TTCL)
US-10-625-047-27

Query Match 95.3%; Score 1079; DB 16; Length 218;
Best Local Similarity 95.9%; Pred. No. 2.1e-83;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy	1 RSAVVTQESALTSPGETVLTCSRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRapg 60
Db	1 RSAVVTQESALTSPGETVLTCSRSTGAVTTSNYANWVQEKPDLFTGLIGGNNNRppg 60
Qy	61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
Db	61 VPARFSGSLIGDKAALTIAQTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120
Qy	121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLs 180
Db	121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLs 180
Qy	181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
Db	181 STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFRGEC 218

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:22:51 ; Search time 25.5 Seconds
(without alignments)
822.559 Million cell updates/sec

Title: US-09-671-953B-5

Perfect score: 1132

Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	740	65.4	215	2	JE0242	Ig kappa chain NIG
2	729	64.4	215	2	JE0244	Ig kappa chain NIG
3	724.5	64.0	214	2	PC4156	Ig lambda chain V
4	716	63.3	215	2	JE0243	Ig kappa chain NIG
5	682.5	60.3	216	2	JE0241	Ig kappa chain Am3
6	675	59.6	215	2	A23746	Ig kappa chain V-I
7	578.5	51.1	135	2	S52059	JC-kappa protein -
8	552.5	48.8	240	2	S06084	Ig kappa chain pre
9	544	48.1	106	1	K3HU	Ig kappa chain C r
10	543.5	48.0	287	4	PC4402	pelB leader/Ig hea
11	537	47.4	128	2	S52450	Ig lambda chain V
12	530.5	46.9	220	2	A31790	Ig kappa chain V r
13	529	46.7	129	1	L1MS4E	Ig lambda-1 chain

14	522	46.1	235	2	S25058	Ig kappa chain - m
15	521	46.0	113	2	S06819	Ig lambda chain V
16	519.5	45.9	112	2	S06818	Ig lambda chain V
17	517	45.7	106	2	S20654	Ig lambda chain V
18	515	45.5	219	2	S38865	Ig kappa chain - m
19	514	45.4	225	2	S37484	Ig kappa chain - m
20	509.5	45.0	114	2	S06820	Ig lambda chain V
21	509.5	45.0	234	2	S14237	Ig kappa chain pre
22	509	45.0	99	2	A37927	Ig kappa chain C r
23	506.5	44.7	230	2	S33161	Ig kappa chain - s
24	503.5	44.5	218	2	S68241	Ig kappa chain V r
25	503	44.4	99	2	S26653	Ig kappa chain C r
26	501.5	44.3	214	2	S68212	Ig kappa chain (Ma
27	499.5	44.1	225	2	JL0029	Ig kappa chain pre
28	498.5	44.0	218	2	JC5810	monoclonal antibod
29	497.5	43.9	234	2	S01320	Ig kappa chain pre
30	495.5	43.8	114	2	S06822	Ig lambda chain V
31	495	43.7	113	2	B54256	Ig lambda-1 chain
32	492	43.5	217	2	S42772	Ig kappa chain - m
33	492	43.5	219	2	S16112	Ig kappa chain V r
34	491	43.4	129	1	L2MS35	Ig lambda-2 chain
35	488.5	43.2	219	2	PC4203	Ig kappa chain (mo
36	485	42.8	235	2	S25749	Ig lambda chain -
37	484.5	42.8	99	2	PH1089	Ig lambda chain V
38	482	42.6	99	2	S14582	Ig lambda chain V
39	482	42.6	113	2	S06821	Ig lambda chain V
40	482	42.6	219	2	S52028	Ig kappa chain - m
41	477	42.1	97	2	PH1090	Ig lambda chain V
42	477	42.1	116	1	L1MSV	Ig lambda-1 chain
43	475.5	42.0	210	2	A56169	Ig kappa chain V r
44	472	41.7	99	2	S14584	Ig lambda chain V
45	469	41.4	100	2	PH1088	Ig lambda chain V

ALIGNMENTS

RESULT 1
 JE0242
 Ig kappa chain NIG26 precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C;Accession: JE0242
 R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.;
 Shinoda, T.
 submitted to JIPID, November 1998
 A;Description: Structure relationship of kappatype light chains with AL
 amyloidosis: Multiple deletions found in a VkIV protein.
 A;Reference number: JE0241
 A;Accession: JE0242
 A;Molecule type: protein
 A;Residues: 1-215 <ALI>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 740; DB 2; Length 215;
 Best Local Similarity 70.4%; Pred. No. 7.9e-49;

Matches 152; Conservative 17; Mismatches 43; Indels 4; Gaps 3;

Qy 4 VVTQE-SALTTSPGETVLTCSRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPGVP 62
|:|| |: |||| ||:||:| ::|| | :|| :|| ::|| |:|

Db 3 VLTQSPGTLSLSPGERATLSCRAS--QSVSNNYLAWYQQKPGQAPSLLIYDASSRATGIP 60

Qy 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
||||| | ||||:| :|| | :| : | || |||: : |||||||||||

Db 61 DRFSGSGSGTDFILTISGLEPEDFAVYYCQQYDRPPWTFGQGTKVEI-KRTVAAPSVFIF 119

Qy 123 PPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
|||||||||||||||||||||||||||||||||||||||||||||||||

Db 120 PPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179

Qy 183 LTLSKADYEKHKVYACEVTHQGLXPVTKSFNRGEC 218
||||||||||||||||| |||||||||||

Db 180 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFRGEC 215

us-09-671-953b-5.rup

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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:22:03 ; Search time 116.5 Seconds
(without alignments)
958.225 Million cell updates/sec

Title: US-09-671-953B-5

Perfect score: 1132

Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	DB	ID	Description
1	734	64.8	235	2	Q6PJF2	Q6pjf2 homo sapien
2	733	64.8	235	2	Q6GMW0	Q6gmw0 homo sapien
3	732	64.7	236	2	Q6GMW1	Q6gmw1 homo sapien
4	727.5	64.3	236	2	Q7Z3Y4	Q7z3y4 homo sapien
5	727	64.2	234	2	Q7Z473	Q7z473 homo sapien
6	723.5	63.9	236	2	Q6PIH7	Q6pih7 homo sapien
7	722.5	63.8	236	2	Q6GMX9	Q6gmx9 homo sapien
8	721.5	63.7	236	2	Q6P5S8	Q6p5s8 homo sapien
9	721	63.7	235	2	Q6GMV9	Q6gmv9 homo sapien
10	720.5	63.6	236	2	Q6GMX0	Q6gmx0 homo sapien
11	717.5	63.4	236	2	Q6PIL8	Q6pil8 homo sapien
12	715.5	63.2	236	2	Q6GMX8	Q6gmx8 homo sapien
13	704	62.2	236	2	Q6PIT5	Q6pit5 homo sapien
14	702.5	62.1	236	2	Q6PIH4	Q6pih4 homo sapien
15	697	61.6	239	2	Q8TCDO	Q8tcd0 homo sapien
16	696	61.5	240	2	Q6PIH6	Q6pih6 homo sapien
17	694	61.3	239	2	Q8NEKO	Q8nek0 homo sapien
18	666	58.8	239	2	Q6P491	Q6p491 homo sapien
19	564.5	49.9	120	2	Q6P5R5	Q6p5r5 homo sapien
20	544	48.1	106	1	KAC_HUMAN	P01834 homo sapien
21	535	47.3	129	1	LV1E_MOUSE	P01727 mus musculu

us-09-671-953b-5.rup							
22	530	46.8	129	1	LV1D_MOUSE	P01726	mus musculu
23	529	46.7	129	1	LV1B_MOUSE	P01724	mus musculu
24	523	46.2	129	2	Q8VDE2	Q8vde2	mus musculu
25	522.5	46.2	238	2	Q66JS7	Q66js7	mus musculu
26	521	46.0	110	1	LV1C_MOUSE	P01725	mus musculu
27	514.5	45.5	113	2	Q8CGS1	Q8cgs1	mus musculu
28	510.5	45.1	236	2	Q7TS98	Q7ts98	mus musculu
29	507.5	44.8	109	2	Q9ET13	Q9et13	mus musculu
30	502	44.3	219	2	Q65ZC0	Q65zc0	mus musculu
31	497.5	43.9	241	2	Q63ZX4	Q63zx4	mus musculu
32	491	43.4	129	1	LV2B_MOUSE	P01729	mus musculu
33	477	42.1	117	1	LV1A_MOUSE	P01723	mus musculu
34	454	40.1	117	1	LV2A_MOUSE	P01728	mus musculu
35	442.5	39.1	236	2	Q8NEJ1	Q8nej1	homo sapien
36	440	38.9	235	2	Q6IN99	Q6in99	homo sapien
37	435	38.4	248	2	Q7SYU1	Q7syu1	xenopus lae
38	432	38.2	233	2	Q8TBC9	Q8tbc9	homo sapien
39	430.5	38.0	230	2	Q7Z2U3	Q7z2u3	homo sapien
40	430.5	38.0	236	2	Q6PIQ7	Q6piq7	homo sapien
41	428.5	37.9	236	2	Q6GMV7	Q6gmv7	homo sapien
42	428.5	37.9	236	2	Q6IPQ0	Q6ipq0	homo sapien
43	427.5	37.8	234	2	Q7Z2U7	Q7z2u7	homo sapien
44	426.5	37.7	236	2	Q6GMX4	Q6gmx4	homo sapien
45	426	37.6	231	2	Q6GNB8	Q6gnb8	xenopus lae

ALIGNMENTS

RESULT 1

Q6PJF2

ID Q6PJF2 PRELIMINARY; PRT; 235 AA.
 AC Q6PJF2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human

us-09-671-953b-5.rup

RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC016380; AAH16380.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 64.8%; Score 734; DB 2; Length 235;
Best Local Similarity 70.4%; Pred. No. 1.5e-56;
Matches 152; Conservative 18; Mismatches 42; Indels 4; Gaps 3;

Qy	4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPGVP 62
Db	23 VLTQSPATLSLSPGERATLSCRAS--QIVSSAYLAWYQQKPGQAPRLLMFGSSSRATGIP 80
Qy	63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGTKLTVLSRTVAAPSVFIF 122
Db	81 DRFSGSGSGTDFTLTISRLPEDFAVYYCQQYQGSSQGTFGPGTKVDI-KRTVAAPSVFIF 139
Qy	123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLST 182
Db	140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLST 199
Qy	183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
Db	200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFRGEC 235

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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:19:05 ; Search time 120 Seconds
(without alignments)
702.615 Million cell updates/sec

Title: US-09-671-953B-7

Perfect score: 1134

Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query						Description
No.	Score	Match	Length	DB	ID		
1	1132	99.8	218	4	AAB20360		Aab20360 Anti-chel
2	1122	98.9	218	4	AAB20359		Aab20359 Anti-chel
3	1113	98.1	218	4	AAB20358		Aab20358 Anti-chel
4	1083	95.5	218	8	ADQ98050		Adq98050 Chimeric
5	1082	95.4	218	8	ADQ98051		Adq98051 Chimeric
6	779	68.7	215	8	ADR23362		Adr23362 Human CD7
7	759.5	67.0	235	5	AAE27925		Aae27925 Human C2B
8	759.5	67.0	235	6	ABB82834		Abb82834 Antibody
9	759	66.9	213	8	ADL92471		Adl92471 Antibody

10	757	66.8	235	2	AAW82740	Aaw82740 Plasmid p
11	754.5	66.5	235	3	AAB08025	Aab08025 A dimeric
12	753	66.4	213	6	AAE34878	Aae34878 BIWA4/8 a
13	753	66.4	213	8	ADL15445	Adl15445 Humanised
14	753	66.4	213	8	ADO00853	Ado00853 Humanised
15	751	66.2	213	6	AAE35326	Aae35326 Humanised
16	751	66.2	213	6	AAE34877	Aae34877 BIWA4 ant
17	751	66.2	213	8	ADL15441	Adl15441 Humanised
18	751	66.2	213	8	ADO00849	Ado00849 Humanised
19	751	66.2	236	8	ADP79579	Adp79579 Chimeric
20	750	66.1	220	2	AAW07528	Aaw07528 Anti-HGF
21	746	65.8	215	8	ADQ31891	Adq31891 Antibody
22	744	65.6	215	8	ADQ31885	Adq31885 Antibody
23	743.5	65.6	234	5	AAO14066	Aao14066 Light cha
24	743.5	65.6	234	6	ABU08018	Abu08018 Human mon
25	743.5	65.6	234	7	ADF65776	Adf65776 Human mon
26	743.5	65.6	234	8	ADJ92516	Adj92516 Human SOJ
27	743	65.5	233	3	AYY93704	Aay93704 The kappa
28	743	65.5	233	3	AYY93731	Aay93731 The kappa
29	743	65.5	233	6	AAE35886	Aae35886 Human 4.8
30	743	65.5	239	8	ADK70470	Adk70470 Respirato
31	741.5	65.4	240	6	ABJ38595	Abj38595 Hepatitis
32	741	65.3	213	2	AAW05830	Aaw05830 Humanised
33	740.5	65.3	234	3	AYY92239	Aay92239 Human bon
34	739.5	65.2	234	6	ABP55483	Abp55483 CJRA05 pr
35	739	65.2	215	8	ADQ16702	Adq16702 Modified
36	738	65.1	213	6	AAE33521	Aae33521 Human AQC
37	738	65.1	232	8	ADP79583	Adp79583 2H7.v16 L
38	736	64.9	235	2	AAW06180	Aaw06180 Humanised
39	736	64.9	236	2	AYY34096	Aay34096 Partial a
40	735.5	64.9	214	8	ADH34591	Adh34591 023 light
41	735.5	64.9	349	2	AAR12128	Aar12128 1B1 IgG a
42	735.5	64.9	414	2	AAR13111	Aar13111 1B1 IgG a
43	735.5	64.9	414	2	AAR13018	Aar13018 1B1 IgG a
44	735	64.8	213	4	AAB83157	Aab83157 Gangliosi
45	735	64.8	215	6	ABR01469	Abr01469 Human ant

ALIGNMENTS

RESULT 1

AAB20360

ID AAB20360 standard; protein; 218 AA.

XX

AC AAB20360;

XX

DT 11-JUN-2001 (first entry)

XX

DE Anti-chelate antibody CHA255 light chain mutant S95C.

XX

KW Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour;
KW cancer; therapy; mutant; mutein.

XX

OS Mus musculus.

OS Synthetic.

XX

FH Key Location/Qualifiers
FT Region 1. .23
FT /label= FR1
FT /note= "framework region 1"
FT Region 24. .37
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 38. .52
FT /label= FR2
FT /note= "framework region 2"
FT Region 53. .59
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 60. .92
FT /label= FR3
FT /note= "framework region 3"
FT Region 93. .100
FT /label= CDR3
FT /note= "complementarity determining region 3"
FT Misc-difference 95
FT /note= "replaces Ser of wild-type sequence"
FT Misc-difference 100
FT /note= "encoded by GTR"
FT Region 101. .131
FT /label= FR4
FT /note= "framework region 4"
FT Misc-difference 112
FT /note= "encoded by CGW"
FT Misc-difference 113
FT /note= "encoded by ACK"
FT Misc-difference 206
FT /note= "encoded by AGY"
FT Misc-difference 207
FT /note= "encoded by TYG"
XX
PN WO200122922-A2.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-US026619.
XX
PR 27-SEP-1999; 99US-0156194P.
PR 31-MAY-2000; 2000US-0208684P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Meares C, Chmura A;
XX
DR WPI; 2001-244971/25.
DR N-PSDB; AAF30635.
XX
PT Nucleic acid encoding a mutant antibody comprising a reactive site that
PT specifically binds to a metal chelate useful as analytical agents and in
PT clinical diagnosis, as well as in the treatment of disease, particularly
PT cancer.
XX
PS Disclosure; Fig 14; 100pp; English.

XX

CC The invention provides a mutant antibody comprising a reactive site that
CC is not present in the wild-type of the antibody. The antibody also has a
CC complementarity determining region (CDR) that specifically binds to a
CC metal chelate against which the wild-type antibody is raised. The
CC reactive site of the mutant antibody is in a position proximate to or
CC within the CDR, such that the chelate and the antibody are able to form a
CC covalent bond. The present sequence is that of the light chain variable
CC region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C
CC mutation. As an example of the method of the invention, rational computer
CC -aided design was used to develop an indium-EDTA chelate to covalently
CC bind to CHA255 in vivo. The premise was to allow the chelate to bind non-
CC covalently to CHA255 bound to a tumour and then to covalently attach the
CC chelate to the antibody, thereby trapping it at the tumour site. This
CC involved cloning the variable domains of CHA255 to construct a
CC human/mouse chimeric Fab fragment that could be expressed in Escherichia
CC coli, and the synthesis and screening of benzyl-EDTA chelates carrying
CC weakly electrophilic groups capable of conjugation of the antibody in
CC vivo. This Fab can be conjugated to a targeting moiety when desired. A
CC reactive site was incorporated into the antibody by engineering a Cys
CC residue at location Asn-96 or Ser-95 of the light chain, near the region
CC of the antibody to which the chelate bound. This was accomplished by site
CC -directed mutagenesis of a nucleic acid encoding the wild-type of the
CC anti-chelate antibody

XX

SQ Sequence 218 AA;

Query Match 99.8%; Score 1132; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.9e-79;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPG 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPG 60

Qy 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120

Qy 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180

Qy 181 STLTLSKADYEKKVYACEVTHQGLSXPVTKSFNRGEC 218

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 STLTLSKADYEKKVYACEVTHQGLSXPVTKSFNRGEC 218

us-09-671-953b-7.rai

GenCore version 5.1.6
copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2005, 15:23:21 ; Search time 30 Seconds
(without alignments)
542.450 Million cell updates/sec

Title: US-09-671-953B-7

Perfect score: 1134

Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	757	66.8	235	3	US-09-423-439-18	Sequence 18, Appl
2	750	66.1	220	3	US-08-952-235-1	Sequence 1, Appl
3	750	66.1	220	4	US-09-669-971-1	Sequence 1, Appl
4	743	65.5	233	4	US-09-472-087-15	Sequence 15, Appl
5	743	65.5	233	4	US-09-472-087-67	Sequence 67, Appl
6	739	65.2	213	3	US-08-397-411-12	Sequence 12, Appl
7	736	64.9	235	4	US-09-011-769A-27	Sequence 27, Appl
8	734	64.7	236	4	US-09-315-926A-79	Sequence 79, Appl
9	732.5	64.6	234	4	US-09-472-087-17	Sequence 17, Appl
10	732.5	64.6	234	4	US-09-472-087-69	Sequence 69, Appl
11	732	64.6	235	4	US-09-472-087-14	Sequence 14, Appl
12	732	64.6	235	4	US-09-472-087-65	Sequence 65, Appl
13	731.5	64.5	224	4	US-09-456-090A-84	Sequence 84, Appl
14	731.5	64.5	224	4	US-09-453-234-84	Sequence 84, Appl
15	730.5	64.4	491	4	US-10-011-125A-2	Sequence 2, Appl
16	728.5	64.2	214	3	US-08-397-411-5	Sequence 5, Appl
17	728	64.2	239	4	US-09-627-896B-22	Sequence 22, Appl

us-09-671-953b-7.ra1						
18	726.5	64.1	214	4	US-09-472-087-71	Sequence 71, Appl
19	726.5	64.1	224	4	US-09-456-090A-46	Sequence 46, Appl
20	726.5	64.1	224	4	US-09-453-234-46	Sequence 46, Appl
21	725	63.9	234	4	US-09-740-002-26	Sequence 26, Appl
22	724.5	63.9	234	4	US-09-740-002-24	Sequence 24, Appl
23	724	63.8	214	1	US-08-458-516-12	Sequence 12, Appl
24	724	63.8	235	3	US-09-171-945-17	Sequence 17, Appl
25	722.5	63.7	224	4	US-09-456-090A-36	Sequence 36, Appl
26	722.5	63.7	224	4	US-09-453-234-36	Sequence 36, Appl
27	722.5	63.7	226	4	US-09-456-090A-74	Sequence 74, Appl
28	722.5	63.7	226	4	US-09-453-234-74	Sequence 74, Appl
29	722	63.7	233	3	US-09-485-737B-69	Sequence 69, Appl
30	722	63.7	233	4	US-10-071-485-69	Sequence 69, Appl
31	721.5	63.6	218	5	PCT-US96-13152-2	Sequence 2, Appl
32	721.5	63.6	236	1	US-08-157-101A-5	Sequence 5, Appl
33	720.5	63.5	213	3	US-08-630-820-6	Sequence 6, Appl
34	720.5	63.5	213	4	US-09-273-453-6	Sequence 6, Appl
35	719	63.4	219	3	US-09-027-449-72	Sequence 72, Appl
36	719	63.4	219	3	US-09-026-985-72	Sequence 72, Appl
37	719	63.4	219	4	US-09-121-952A-72	Sequence 72, Appl
38	719	63.4	219	4	US-09-234-340A-72	Sequence 72, Appl
39	719	63.4	235	3	US-09-171-945-97	Sequence 97, Appl
40	719	63.4	242	3	US-09-027-449-56	Sequence 56, Appl
41	719	63.4	242	3	US-08-804-444A-56	Sequence 56, Appl
42	719	63.4	242	3	US-09-026-985-56	Sequence 56, Appl
43	719	63.4	242	4	US-09-121-952A-56	Sequence 56, Appl
44	719	63.4	242	4	US-09-234-340A-56	Sequence 56, Appl
45	718.5	63.4	214	3	US-09-247-352-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-423-439-18

; Sequence 18, Application US/09423439
Patent No. 6339070

GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles
BLAKELY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997

us-09-671-953b-7.raii

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-423-439-18

Query Match 66.8%; Score 757; DB 3; Length 235;
Best Local Similarity 71.8%; Pred. No. 7.9e-67;
Matches 155; Conservative 15; Mismatches 40; Indels 6; Gaps 3;

DB 25 VLSQSPAILSASPGEKVMTCRAS----SSVTYIHWWQQKPGSSPKSWIYATSNL��GPV 80

QY 63 ARFGSGLIGDKAALITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122

Pb 81 ARFSGSGSGTSYSLTISRVEAEDAATYYCOHWSSKPPTFGGGKLEI-KRTVAAPSVIF 139

QY 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182

183. LTLSKADYEHKVVACFVTHOGLSXPRVTKSENRGEC 218

QY 183 LILSKADYEHKRVYACEVTHQGLSAPVIRSFNRGEL 210

Qy 183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Db 200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235

us-09-671-953b-7.rapb

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:34:17 ; Search time 113.5 Seconds
(without alignments)
802.937 Million cell updates/sec

Title: US-09-671-953B-7

Perfect score: 1134

Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	.1083	95.5	218	16	US-10-625-047-27	Sequence 27, Appl

us-09-671-953b-7.rabp							
2	1083	95.5	218	17	US-10-631-258-27	Sequence 27, Appl	
3	1083	95.5	218	18	US-10-350-555-27	Sequence 27, Appl	
4	1082	95.4	218	16	US-10-625-047-28	Sequence 28, Appl	
5	1082	95.4	218	17	US-10-631-258-28	Sequence 28, Appl	
6	1082	95.4	218	18	US-10-350-555-28	Sequence 28, Appl	
7	759.5	67.0	235	16	US-10-723-003-42	Sequence 42, Appl	
8	759.5	67.0	235	20	US-11-004-639-42	Sequence 42, Appl	
9	759	66.9	213	17	US-10-822-231-3	Sequence 3, Appl	
10	759	66.9	213	18	US-10-880-028-49	Sequence 49, Appl	
11	759	66.9	213	18	US-10-880-320-49	Sequence 49, Appl	
12	754.5	66.5	235	20	US-11-019-180-2	Sequence 2, Appl	
13	753	66.4	213	14	US-10-150-475A-8	Sequence 8, Appl	
14	753	66.4	213	16	US-10-704-522-8	Sequence 8, Appl	
15	753	66.4	213	16	US-10-645-215-8	Sequence 8, Appl	
16	753	66.4	213	20	US-11-136-538-9	Sequence 9, Appl	
17	751	66.2	213	14	US-10-150-475A-4	Sequence 4, Appl	
18	751	66.2	213	16	US-10-704-522-4	Sequence 4, Appl	
19	751	66.2	213	16	US-10-645-215-4	Sequence 4, Appl	
20	751	66.2	213	20	US-11-136-538-8	Sequence 8, Appl	
21	750	66.1	220	9	US-09-995-693-1	Sequence 1, Appl	
22	750	66.1	220	14	US-10-232-408-1	Sequence 1, Appl	
23	746	65.8	215	17	US-10-724-274-32	Sequence 32, Appl	
24	746	65.8	215	18	US-10-830-956-32	Sequence 32, Appl	
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26	745	65.7	213	17	US-10-822-300-135	Sequence 135, App	
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28	744	65.6	215	17	US-10-822-300-141	Sequence 141, App	
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33	743.5	65.6	234	15	US-10-461-148-2	Sequence 2, Appl	
34	743	65.5	233	14	US-10-153-382-11	Sequence 11, Appl	
35	743	65.5	233	16	US-10-612-497-15	Sequence 15, Appl	
36	743	65.5	233	16	US-10-612-497-67	Sequence 67, Appl	
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38	743	65.5	233	16	US-10-776-649-67	Sequence 67, Appl	
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40	743	65.5	233	20	US-11-085-368-47	Sequence 47, Appl	
41	739.5	65.2	234	15	US-10-045-674-587	Sequence 587, App	
42	739	65.2	215	15	US-10-307-724-122	Sequence 122, App	
43	739	65.2	215	16	US-10-737-290-122	Sequence 122, App	
44	739	65.2	239	16	US-10-737-290-142	Sequence 142, App	
45	738	65.1	213	15	US-10-474-832-3	Sequence 3, Appl	

ALIGNMENTS

RESULT 1

US-10-625-047-27

Sequence 27, Application us/10625047

Publication No. US20040198962A1

GENERAL INFORMATION:

APPLICANT: Meares, Claude

APPLICANT: Corneillie, Todd

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Multi-Functional Antibodies

FILE REFERENCE: 023070-130910us

CURRENT APPLICATION NUMBER: US/10/625,047

CURRENT FILING DATE: 2003-07-22

PRIOR APPLICATION NUMBER: US 10/350,555

PRIOR FILING DATE: 2003-01-23

NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 218
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:native cloned
OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region
OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody
OTHER INFORMATION: kappa light chain constant region (TTCL)
US-10-625-047-27

Query Match 95.5%; Score 1083; DB 16; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.2e-84;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 RSAVVTQESALTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRPG 60
Db 1 RSAVVTQESALTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDLFTGLIGGNNRPPG 60
Qy 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
Db 61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120
Qy 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
Db 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
Qy 181 STLTLSKADYEHKVYACEVTHQGLSXPVTKSFNRGEC 218
Db 181 STLTLSKADYEHKVYACEVTHQGLSLPVTKSFNRGEC 218

RESULT 2

US-10-631-258-27

Sequence 27, Application US/10631258
Publication No. US20050026263A1
GENERAL INFORMATION:
APPLICANT: Meares, Claude
APPLICANT: Corneillie, Todd
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Multi-Functional Antibodies
FILE REFERENCE: 023070-130920US
CURRENT APPLICATION NUMBER: US/10/631,258
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US 10/350,555
PRIOR FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: US 10/625,047
PRIOR FILING DATE: 2003-07-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 218
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:native cloned
OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region
OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody
OTHER INFORMATION: kappa light chain constant region (TTCL)
US-10-631-258-27

Db 181 |||||||STLTL SKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218

RESULT 4

US-10-625-047-28

Sequence 28, Application US/10625047

Publication No. US20040198962A1

GENERAL INFORMATION:

APPLICANT: Meares, Claude

APPLICANT: Corneillie, Todd

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Multi-Functional Antibodies

FILE REFERENCE: 023070-130910US

CURRENT APPLICATION NUMBER: US/10/625,047

CURRENT FILING DATE: 2003-07-22

PRIOR APPLICATION NUMBER: US 10/350,555

PRIOR FILING DATE: 2003-01-23

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 28

LENGTH: 218

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:N53C cloned

OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable

OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin

OTHER INFORMATION: antibody kappa light chain constant region (TTCL)

US-10-625-047-28

Query Match 95.4%; Score 1082; DB 16; Length 218;
 Best Local Similarity 95.9%; Pred. No. 1.5e-84;
 Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRPG 60
 |||||||STLTL SKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218

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Qy 61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
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Qy 121 IFPPSDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
 |||||||STLTL SKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218

Db 121 IFPPSDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180

Qy 181 STLTL SKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218

Db 181 STLTL SKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218

RESULT 5

US-10-631-258-28

Sequence 28, Application US/10631258

Publication No. US20050026263A1

GENERAL INFORMATION:

APPLICANT: Meares, Claude

APPLICANT: Corneillie, Todd

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Multi-Functional Antibodies

FILE REFERENCE: 023070-130920US

CURRENT APPLICATION NUMBER: US/10/631,258

CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US 10/350,555
PRIOR FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: US 10/625,047
PRIOR FILING DATE: 2003-07-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 218
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:N53C cloned
OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable
OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin
OTHER INFORMATION: antibody kappa light chain constant region (TTCL)
US-10-631-258-28

Query Match 95.4%; Score 1082; DB 17; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.5e-84;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy	1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRapg 60
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Qy	61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
Db	61 VPARFSGSLIGDKAALTIAQTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120
Qy	121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
Db	121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
Qy	181 STLTLSKADYEKHKVYACEVTHQGLXPVTKSFNRGEC 218
Db	181 STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218

RESULT 6

US-10-350-555-28
Sequence 28, Application US/10350555
Publication No. US20040146934A1
GENERAL INFORMATION:
APPLICANT: Meares, Claude
APPLICANT: Corneillie, Todd
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Multi-Functional Antibodies
FILE REFERENCE: 023070-130900US
CURRENT APPLICATION NUMBER: US/10/350,555
CURRENT FILING DATE: 2003-01-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 218
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:N53C cloned
OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable
OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin
OTHER INFORMATION: antibody kappa light chain constant region (TTCL)
US-10-350-555-28

us-09-671-953b-7.rapb

Query Match 95.4%; Score 1082; DB 18; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.5e-84;
Matches 209; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy	1 RSAVVTQESALTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPG 60
Db	1 RSAVVTQESALTSPGETVTLCRSSTGAVTTSNYANWVQEKPDLFTGLIGGCNNRPPG 60
Qy	61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
Db	61 VPARFSGSLIGDKAALTIACTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120
Qy	121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
Db	121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 180
Qy	181 STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
Db	181 STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218

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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:22:51 ; Search time 25.5 Seconds
(without alignments)
822.559 Million cell updates/sec

Title: US-09-671-953B-7

Perfect score: 1134

Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	739	65.2	215	2	JE0242	Ig kappa chain NIG
2	735	64.8	215	2	JE0244	Ig kappa chain NIG
3	728.5	64.2	214	2	PC4156	Ig lambda chain V
4	721	63.6	215	2	JE0243	Ig kappa chain NIG
5	678.5	59.8	216	2	JE0241	Ig kappa chain Am3
6	672	59.3	215	2	A23746	Ig kappa chain V-I
7	578.5	51.0	135	2	S52059	JC-kappa protein -
8	549.5	48.5	240	2	S06084	Ig kappa chain pre
9	547.5	48.3	287	4	PC4402	pelB leader/Ig hea
10	544	48.0	106	1	K3HU	Ig kappa chain C r
11	541	47.7	128	2	S52450	Ig lambda chain V
12	534.5	47.1	220	2	A31790	Ig kappa chain V r
13	533	47.0	129	1	L1MS4E	Ig lambda-1 chain

14	526	46.4	235	2	S25058	Ig kappa chain - m
15	525	46.3	113	2	S06819	Ig lambda chain V
16	523.5	46.2	112	2	S06818	Ig lambda chain V
17	521	45.9	106	2	S20654	Ig lambda chain V
18	513.5	45.3	114	2	S06820	Ig lambda chain V
19	511	45.1	219	2	S38865	Ig kappa chain - m
20	511	45.1	225	2	S37484	Ig kappa chain - m
21	509	44.9	99	2	A37927	Ig kappa chain C r
22	504.5	44.5	234	2	S14237	Ig kappa chain pre
23	503	44.4	99	2	S26653	Ig kappa chain C r
24	502.5	44.3	230	2	S33161	Ig kappa chain - s
25	500	44.1	113	2	B54256	Ig lambda-1 chain
26	499.5	44.0	114	2	S06822	Ig lambda chain V
27	498	43.9	129	1	L2MS35	Ig lambda-2 chain
28	497.5	43.9	214	2	S68212	Ig kappa chain (Ma
29	497.5	43.9	218	2	S68241	Ig kappa chain V r
30	495.5	43.7	225	2	JL0029	Ig kappa chain pre
31	495.5	43.7	234	2	S01320	Ig kappa chain pre
32	492.5	43.4	218	2	JC5810	monoclonal antibod
33	490	43.2	217	2	S42772	Ig kappa chain - m
34	488.5	43.1	99	2	PH1089	Ig lambda chain V
35	488	43.0	219	2	S16112	Ig kappa chain V r
36	486	42.9	99	2	S14582	Ig lambda chain V
37	486	42.9	113	2	S06821	Ig lambda chain V
38	485	42.8	235	2	S25749	Ig lambda chain -
39	484.5	42.7	219	2	PC4203	Ig kappa chain (mo
40	478	42.2	97	2	PH1090	Ig lambda chain V
41	478	42.2	116	1	L1MSV	Ig lambda-1 chain
42	478	42.2	219	2	S52028	Ig kappa chain - m
43	473	41.7	99	2	S14584	Ig lambda chain V
44	473	41.7	100	2	PH1088	Ig lambda chain V
45	469.5	41.4	210	2	A56169	Ig kappa chain V r

ALIGNMENTS

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C;Species: Homo sapiens (man)

C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C;Accession: JE0242

R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998

A;Description: Structure relationship of kappatype light chains with AL

amyloidosis: Multiple deletions found in a VkIV protein.

A;Reference number: JE0241

A;Accession: JE0242

A;Molecule type: protein

A;Residues: 1-215 <ALI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 739; DB 2; Length 215;
 Best Local Similarity 70.4%; Pred. No. 1.4e-48;

Matches 152; Conservative 17; Mismatches 43; Indels 4; Gaps 3;

Qy 4 VVTQE-SALTTSPGETVLTCCRSSIGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPGVP 62
|:|| |: |||| ||:||:|| ::|| | :|| :|| :|| |:||
Db 3 VLTQSPGTLSLSPGERATLSCRAS--QSVSNNYLAWYQQKPGQAPSLLIYDASSRATGIP 60

Qy 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
||||| | |||:| :|| | :| : | || ||:| : |||||||||||
Db 61 DRFSGSGSGTDFILTISGLEPEDFAVYYCQQYDRPPWTFGQGTKVEI-KRTVAAPSVFIF 119

Qy 123 PPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 182
|||||||||||||||||||||||||||||||||||||||||||||
Db 120 PPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 179

Qy 183 LTLSKADYEHKVYACEVTHQGLSPVTKSFNRGEC 218
||||||||||||||||| |||||||
Db 180 LTLSKADYEHKVYACEVTHQGLSSPVTKSFRGEC 215

us-09-671-953b-7.rup

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OM protein - protein search, using sw model

Run on: October 28, 2005, 15:22:03 ; Search time 116.5 Seconds
(without alignments)
958.225 Million cell updates/sec

Title: US-09-671-953B-7

Perfect score: 1134

Sequence: 1 RSAVVTQESALTTSPGETVT.....EVTHQGLSXPVTKSFNRGEC 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	DB	ID	Description
1	732	64.6	235	2	Q6GMW0	Q6gmw0 homo sapien
2	731	64.5	235	2	Q6PJF2	Q6pjf2 homo sapien
3	728	64.2	236	2	Q6GMW1	Q6gmw1 homo sapien
4	725	63.9	234	2	Q7Z473	Q7z473 homo sapien
5	722.5	63.7	236	2	Q7Z3Y4	Q7z3y4 homo sapien
6	721	63.6	235	2	Q6GMV9	Q6gmv9 homo sapien
7	720.5	63.5	236	2	Q6GMX9	Q6gmx9 homo sapien
8	720.5	63.5	236	2	Q6PIH7	Q6pih7 homo sapien
9	719.5	63.4	236	2	Q6P5S8	Q6p5s8 homo sapien
10	717.5	63.3	236	2	Q6PIL8	Q6pil8 homo sapien
11	714.5	63.0	236	2	Q6GMX0	Q6gmx0 homo sapien
12	709.5	62.6	236	2	Q6GMX8	Q6gmx8 homo sapien
13	706.5	62.3	236	2	Q6PIH4	Q6pih4 homo sapien
14	699	61.6	236	2	Q6PIT5	Q6pit5 homo sapien
15	695	61.3	240	2	Q6PIH6	Q6pih6 homo sapien
16	692	61.0	239	2	Q8NEKO	Q8nek0 homo sapien
17	692	61.0	239	2	Q8TCDO	Q8tcd0 homo sapien
18	663	58.5	239	2	Q6P491	Q6p491 homo sapien
19	564.5	49.8	120	2	Q6P5R5	Q6p5r5 homo sapien
20	544	48.0	106	1	KAC_HUMAN	P01834 homo sapien
21	539	47.5	129	1	LV1E_MOUSE	P01727 mus musculu

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22	534	47.1	129	1	LV1D_MOUSE	P01726	mus musculu
23	533	47.0	129	1	LV1B_MOUSE	P01724	mus musculu
24	527	46.5	129	2	Q8VDE2	Q8vde2	mus musculu
25	525	46.3	110	1	LV1C_MOUSE	P01725	mus musculu
26	518.5	45.7	113	2	Q8CGS1	Q8cgs1	mus musculu
27	516.5	45.5	238	2	Q66JS7	Q66js7	mus musculu
28	512.5	45.2	109	2	Q9ET13	Q9et13	mus musculu
29	505.5	44.6	236	2	Q7TS98	Q7ts98	mus musculu
30	498	43.9	129	1	LV2B_MOUSE	P01729	mus musculu
31	498	43.9	219	2	Q65ZC0	Q65zc0	mus musculu
32	493.5	43.5	241	2	Q63ZX4	Q63zx4	mus musculu
33	478	42.2	117	1	LV1A_MOUSE	P01723	mus musculu
34	450	39.7	117	1	LV2A_MOUSE	P01728	mus musculu
35	441.5	38.9	236	2	Q8NEJ1	Q8nej1	homo sapien
36	440	38.8	235	2	Q6IN99	Q6in99	homo sapien
37	434	38.3	248	2	Q7SYU1	Q7syu1	xenopus lae
38	432.5	38.1	236	2	Q6IPQ0	Q6ipq0	homo sapien
39	430.5	38.0	236	2	Q6PIQ7	Q6piq7	homo sapien
40	430	37.9	233	2	Q8TBC9	Q8tbc9	homo sapien
41	428.5	37.8	230	2	Q7Z2U3	Q7z2u3	homo sapien
42	427.5	37.7	236	2	Q6GMV7	Q6gmv7	homo sapien
43	425.5	37.5	234	2	Q7Z2U7	Q7z2u7	homo sapien
44	424	37.4	231	2	Q6GNB8	Q6gnb8	xenopus lae
45	424	37.4	233	2	Q8N5F4	Q8n5f4	homo sapien

ALIGNMENTS

RESULT 1

Q6GMW0

ID Q6GMW0 PRELIMINARY; PRT; 235 AA.
 AC Q6GMW0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human

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